



(1) GENERAL INFORMATION:

- (i) APPLICANT: Simons, Michael  
Volk, Rudiger  
Horowitz, Arie
- (ii) TITLE OF INVENTION: Stimulation of angiogenesis  
via enhanced endothelial expression of syndecan-4  
core proteins
- (iii) NUMBER OF SEQUENCES: 24
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: David Prashker, Esq.  
(B) STREET: P.O. Box 5387  
(C) CITY: Magnolia  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) ZIP: 01930

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
(B) COMPUTER: Dell PC  
(C) OPERATING SYSTEM: MS DOS  
(D) SOFTWARE: Microsoft Word version 97

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/145,916  
(B) FILING DATE: September 2, 1998  
(C) CLASSIFICATION: Unknown

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: David Prashker, Esq.  
(B) REGISTRATION NUMBER: 29,693  
(C) REFERENCE/DOCKET NUMBER: BIS-039

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (978) 525-3794

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGACGTG CGGCGCTCTG GCTTTGGCTC TGCGCGCTGG CGCTGCGCCT GCAGCCTGCC 60  
CTCCCGCAAA TTGTCACCGC AAATGTGCCT CCTGAAGACC AAGATGGCTC TGGGGACGAC 120  
TCAGACAAC TCTCTGGCTC AGGCACAGGT GCTTTGCCAG ATATGACTTT GTCACGGCAG 180  
ACACCTTCCA CTTGGAAGGA TGTGTGGCTC CTGACAGCTA CACCCACAGC TCCAGAACCC 240  
ACCAGCAGGG ATACCGAGGC CACCCTCACC TCTATCCTGC CGGCTGGAGA GAAGCCTGAG 300  
GAGGGAGAGC CCGTGGCCCA CGTGGAAGCA GAGCCTGACT TCACTGCTCG GGACAAGGAG 360  
AAGGAGGCCA CCACCAGGCC TAGGGAGACC ACACAGCTCC CAGTCACCCA ACAGGCCTCA 420  
ACAGCAGCCA GAGCCACCAC GGCCCAGGCA TCTGTACAGT CTCATCCCCA CGGGGATGTG 480  
CAACCTGGCC TCCACGAGAC CTTGGCTCCC ACAGCACCCG GCCAACCTGA CCATCAGCCT 540  
CCAAGTGTGG AGGATGGAGG CACTTCTGTC ATCAAAGAGG TTGTGGAGGA TGAACTACC 600  
AATCAGCTTC CTGCAGGAGA GGGCTCTGGA GAACAAGACT TCACCTTTGA AACATCTGGG 660  
GAGAACACAG CTGTGGCTGG CGTCGAGCCT GACCTTCGGA ATCAGTCCCC AGTGGATGAA 720  
GGAGCCACAG GTGCTTCTCA GGGCCTTTTG GACAGGAAGG AA 762

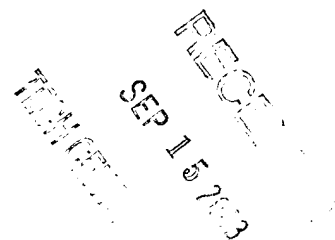
(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCAGGAGGG AGGGAGCCAG AGGAAAAGAA GAGGAGGAGA AGGAGGAGGA CCCGGGGAGG 60



GAGGCGCGGC GCGGGAGGAG GAGGGGCGCA GCCGCGGAGC CAGTGGCCCC GCTTGGACGC 120  
GCTGCTCTCC AGATACCCCC GGAGCTCCAG CCGCGCGGAT CGCGCGCTCC CGCCGCTCTG 180  
CCCCTAAACT TCTGCCGTAG CTCCCTTTCA AGCCAGCGAA TTTATTCTTT AAAACCAGAA 240  
ACTGAACCTC GGCACGGGAA AGGAGTCCGC GGAGGAGCAA AACCACAGCA GAGCAAGAAG 300  
AGCTTCAGAG AGCAGCCTTC CCGGAGCACC AACTCCGTGT CGGGAGTGCA GAAACCAACA 360  
AGTGAGAGGG CGCCGCGTTC CCGGGGCGCA GCTGCGGGCG GCGGGAGCAG GCGCAGGAGG 420  
AGGAAGCGAG CGCCCCGAG CCCCAGAGCC GAGTCCCCGA GCCTGAGCCG CAATCGCTGC 480  
GGTACTCTGC TCCGGATTCTG TGTGCGCGGG CTCGCCGAGC GCTGGGCAGG AGGCTTCGTT 540  
TTGCCCTGGT TGCAAGCAGC GGCTGGGAGC AGCCGGTCCC TGGGGAATAT GCGGCGCGCG 600  
TGGATCCTGC TCACCTTGGG CTTGGTGGCC TGCGTGTCTG CGGAGTCGAG AGCAGAGCTG 660  
ACATCTGATA AAGACATGTA CCTTGACAAC AGCTCCATTG AAGAAGCTTC AGGAGTGTAT 720  
CCTATTGATG ACGATGACTA CGCTTCTGCG TCTGGCTCGG GAGCTGATGA GGATGTAGAG 780  
AGTCCAGAGC TGACAACAAC TCGACCACTT CCAAAGATAC TGTGACTAG TGCTGCTCCA 840  
AAAGTGGAAA CCACGACGCT GAATATACAG AACAAGATAC CTGCTCAGAC AAAGTCACCT 900  
GAAGAACTG ATAAAGAGAA AGTTCACCTC TCTGACTCAG AAAGGAAAAT GGACCCAGCC 960  
GAAGAGGATA CAAATGTGTA TACTGAGAAA CACTCAGACA GTCTGTTTAA ACGGACAGAA 1020

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly	Arg	Arg	Glu	Gly	Ala	Arg	Gly	Lys	Glu	Glu	Glu	Glu	Lys	Glu	Glu
1			5					10						15	
Asp	Pro	Gly	Arg	Glu	Ala	Arg	Arg	Gly	Arg	Arg	Arg	Gly	Ala	Ala	Ala
			20					25					30		
Glu	Pro	Val	Ala	Pro	Leu	Gly	Arg	Ala	Ala	Leu	Gln	Ile	Pro	Pro	Glu
			35				40					45			
Leu	Gln	Pro	Arg	Gly	Ser	Arg	Ala	Pro	Ala	Ala	Leu	Pro	Leu	Asn	Phe
			50			55					60				
Cys	Arg	Ser	Ser	Leu	Ser	Ser	Gln	Arg	Ile	Tyr	Ser	Leu	Lys	Pro	Glu
65				70					75					80	
Thr	Glu	Pro	Arg	His	Gly	Lys	Gly	Val	Arg	Gly	Gly	Ala	Lys	Pro	Gln
				85				90						95	
Gln	Ser	Lys	Lys	Ser	Phe	Arg	Glu	Gln	Pro	Ser	Arg	Ser	Thr	Asn	Ser
			100					105					110		
Val	Ser	Gly	Val	Gln	Lys	Pro	Thr	Ser	Glu	Arg	Ala	Pro	Arg	Ser	Arg
			115				120					125			
Gly	Ala	Ala	Ala	Gly	Gly	Gly	Ser	Arg	Arg	Arg	Arg	Arg	Lys	Arg	Ala
			130			135					140				
Pro	Pro	Ser	Pro	Glu	Pro	Glu	Ser	Pro	Ser	Leu	Ser	Arg	Asn	Arg	Cys
145				150						155					160
Gly	Thr	Leu	Leu	Arg	Ile	Arg	Val	Arg	Gly	Leu	Ala	Glu	Arg	Trp	Ala
				165				170						175	
Gly	Gly	Phe	Val	Leu	Pro	Trp	Leu	Gln	Ala	Ala	Ala	Gly	Ser	Ser	Arg
			180				185					190			
Ser	Leu	Gly	Asn	Met	Arg	Arg	Ala	Trp	Ile	Leu	Leu	Thr	Leu	Gly	Leu
			195			200						205			
Val	Ala	Cys	Val	Ser	Ala	Glu	Ser	Arg	Ala	Glu	Leu	Thr	Ser	Asp	Lys
			210			215					220				
Asp	Met	Tyr	Leu	Asp	Asn	Ser	Ser	Ile	Glu	Glu	Ala	Ser	Gly	Val	Tyr
225				230					235					240	
Pro	Ile	Asp	Asp	Asp	Asp	Tyr	Ala	Ser	Ala	Ser	Gly	Ser	Gly	Ala	Asp
				245			250							255	
Glu	Asp	Val	Glu	Ser	Pro	Glu	Leu	Thr	Thr	Thr	Arg	Pro	Leu	Pro	Lys
			260			265						270			
Ile	Leu	Leu	Thr	Ser	Ala	Ala	Pro	Lys	Val	Glu	Thr	Thr	Thr	Leu	Asn
			275			280						285			

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Ile Gln Asn Lys Ile Pro Ala Gln Thr Lys Ser Pro Glu Glu Thr Asp  
 290 295 300  
 Lys Glu Lys Val His Leu Ser Asp Ser Glu Arg Lys Met Asp Pro Ala  
 305 310 315 320  
 Glu Glu Asp Thr Asn Val Tyr Thr Glu Lys His Ser Asp Ser Leu Phe  
 325 330 335  
 Lys Arg Thr Glu  
 340

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1079 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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GCCCCGCGC GCTGCTGAGC CGTCCTTGCG GCACGSSGAT GCCCGCGGAG CTGCGGCGGCC 60
TCGCGGTGCT GCTGCTGCTG CTCAGCGCCC GCGCAGCGCT GGCTCAGCCG TGGCGCAATG 120
AGAACTACGA GAGGCCGGTG GACCTGGAGG GCTCTGGGGA TGATGATCCC TTTGGGGACG 180
ATGAACTGGA TGACATCTAC TCGGGCTCCG GCTCAGGCTA TTTTGAGCAG GAGTCAGGGT 240
TGGAGACAGC GGTTCAGCCTC ACCACGGACA CGTCCGTCCC ACTGCCCACC ACGGTGGCCG 300
TGCTGCCTGT CACCTTGGTG CAGCCCATGG CAACACCCTT TGAGCTGTTC CCCACAGAGG 360
ACACGTCCCC TGAGCAAACA ACCAGCGTCT TGTATATCCC CAAGATAACA GAAGCACCAG 420
TGATCCCCAG CTGGAACAACA ACCACCGCCA GTACCACTGC CAGTGACTCC CCCAGTACCA 480
CCTCCACCAC CACCACCACG GCTGCTACCA CCACCACAAC CACCACCACC ATCAGCACCA 540
CTGTGGGCCAC CTCCAAGCCC ACCACTACCC AGAGGTTCCCT GCCCCCCTTT GTCACCAAGG 600
CAGCCACCAC CCGGGCCACC ACCCTGGAGA CGCCCACCAC CTCCATCCCT GAAACCAGTG 660
TCCTGACAGA GGTGACCACA TCACGGCTTG TCCCCTCCAG CACAGCCAAG CCGAGGTCCC 720
TGCCAAAACC AAGCACTTCC AGGACTGCAG AACCACGGA AAAAAGCACT GCCTTGCCCTT 780
CCAGCCCCAC CACGCTGCCA CCCACAGAAG CCCCCAGGT GGAGCCAGGG GAGTTGACGA 840
CAGTCCTCGA CAGTGACCTG GAAGTCCCAA CCAGTAGTGG CCCCAGCGGG GACTTTCGAGA 900
TCCAGGAGGA GGAGGAGACA ACTCGTCCTG AGCTGGGCAA TGAGGTGGTG GCAGTGGTGA 960
CACCACCAGC AGCACCAGGG CTGGGCAAGA ATGCAGAGCC GGGGCTCATC GACAACACAA 1020
TAGAGTCGGG CAGCTCGGCT GCTCAGCTCC CCCAGAAAAA CATCCTGGAG AGGAAGGAA 1079

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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ATGGCGCCTG TCTGCCTGTT TGCGCCGCTG CTGCTGTTGC TCCTCGGAGG TTTCCCCGTC 60
GCCCCAGGCG AGTCGATTCT AGAGACTGAG GTCATAGACC CCCAGGACCT CCTGGAAGGC 120
AGATACTTCT CTGGAGCCCT CCCGGACGAT GAAGACGCTG GGGGCCCTGA GCAGGACTCT 180
GACTTTGAGC TGTCGGGTTC CGGAGATCTA GATGACACGG AGGAGCCCAG GACCTTCCCT 240
GAGGTGATTT CACCCTTGGT GCCACTAGAT AACCACATCC CCGAGAATGC CCAGCCTGGC 300
ATCCGTGTCC CCTCAGAGCC CAAGGAATG GAAGAGAATG AGGTCATTCC CAAAAGGGTC 360
CCCTCCGACG TGGGGGATGA CGATGTGTCC AACAAAGTGT CCATGTCCAG CACTTCCCAG 420
GGCAGCAACA TTTTGTAAAG AACTGAG
447

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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ATGGAGCTCC GGGCCCCGAGG CTGGTGGCTG CTGTGCGCGG CCGCCGCGCT AGTCGCCTGC 60
GCCCGCGGGG ACCCCGCCAG CAAGAGCCGG AGCTGCAGCG AAGTCCGCCA GATCTACGGG 120
GCTAAGGGCT TTAGCCTGAG CGACGTGCCC CAGGCAGAGA TCTCGGGAGA GCACCTGCGG 180
ATCTGCCCCC AGGGCTACAC CTGCTGCACC AGTGAGATGG AGGAGAACCT GGCCAACCAC 240
AGCCGGATGG AGCTGGAGAC CGCACTCCAC GACAGCAGCC GTGCCCTGCA GGCTACACTG 300
GCCACCCAGC TGCATGGCAT CGATGACCAC TTCCAGCGCC TGCTGAATGA CTCGGAGCGT 360
ACACTGCAGG ATGCTTTTCC CGGGGCCCTT GGGGACCTGT ACACGCAGAA CACTCGGGCC 420
TTCCGGGACC TGTATGCTGA GCTGCGTCTC TACTACCGAG GGGCCAACCT ACACCTTGAG 480
GAGACACTGG CCGAGTTCTG GGCACGGCTG CTGGAGCGTC TCTTCAAGCA GCTGCACCCC 540
CAGCTTCTGC TGCCCGATGA CTATCTGGAC TGCCTGGGCA AGCAGGCAGA GGCAGTGC GG 600
CCGTTTGGGG ATGCCCTCG AGAACTGCGC CTGAGGGCCA CCCGTGCTTT TGTGGCGGCA 660
CGATCCTTTG TGCAGGGCCT GGGTGTGGCC AGTGACGTAG TCCGAAAGGT GGCCAGGTT 720
CCTCTGGCCC CAGAATGTTT TCGGGCTGTC ATGAAGTTGG TCTACTGTGC CCATTGCCGG 780
GGAGTCCCTG GTGCCCGGCC CTGTCCCAGC TATTGCCGAA ATGTGCTCAA AGGCTGCCTT 840
GCCAACCAGG CCGACCTGGA TGCCGAGTGG AGGAACCTCC TGGACTCCAT GGTGCTCATC 900
ACTGACAAGT TCTGGGGCCC GTCGGGTGCG GAGAATGTCA TTGGCAGTGT GCATATGTGG 960
CTGGCGGAGG CCATCAACGC CCTCCAGGAC AACAAAGGACA CACTCACAGC TAAGGTCATC 1020
CAGGGCTGCG GAAACCCCAA GGTCAATCCC CATGGCTCTG GGCCTGAGGA GAAGCGTCGC 1080
CGTGGCAAAC TGGCACTGCA GGAGAAGTCC TCCACAGGTA CTCTGGA AAA GCTGGTCTCT 1140
GAGGCCAAGG CCCAGCTCCG AGACATTCAG GACTACTGGA TCAGCCTCCC AGGGACACTG 1200
TGTAGTGAGA AGATGGCCAT GAGTCCTGCC AGCGATGACC GCTGCTGGAA TGGGATTTC 1260
AAGGGCCGGT ACCTACCTGA GGTGATGGGT GATGGGCTGG CCAACCAGAT CAACAACCCT 1320
GAAGTGGAGG TGGACATCAC CAAGCCGGAT ATGACCATCC GGCAGCAGAT CATGCAGCTC 1380
AAGATCATGA CCAACCGTTT ACGTGGCGCC TACGGTGGCA ATGATGTGGA CTTCCAGGAT 1440
GCCAGTGATG ACGGCAGTGG CTCCGGCAGC GGTGGCGGAT GCCCAGATGA CGCCTGTGGC 1500
CGGAGGGTCA GCAAGAAGAG CTCCAGCTCC CGGACCCCTT TGACCCATGC CCTCCCCGGC 1560
TTGTCAGAAC AGGAGGGACA GAAGACCTCG 1590

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala
1          5          10          15
Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
20          25          30
Ser Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
35          40          45
Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
50          55          60
Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn His
65          70          75          80
Ser Arg Met Glu Leu Glu Thr Ala Leu His Asp Ser Ser Arg Ala Leu
85          90          95
Gln Ala Thr Leu Ala Thr Gln Leu His Gly Ile Asp Asp His Phe Gln
100          105          110
Arg Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Asp Ala Phe Pro Gly
115          120          125
Ala Phe Gly Asp Leu Tyr Thr Gln Asn Thr Arg Ala Phe Arg Asp Leu
130          135          140
Tyr Ala Glu Leu Arg Leu Tyr Tyr Arg Gly Ala Asn Leu His Leu Glu
145          150          155          160
Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys
165          170          175
Gln Leu His Pro Gln Leu Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu
180          185          190
Gly Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Asp Ala Pro Arg Glu

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195	200	205
Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val		
210	215	220
Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val		
225	230	235
Pro Leu Ala Pro Glu Cys Ser Arg Ala Val Met Lys Leu Val Tyr Cys		240
	245	250
Ala His Cys Arg Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys		255
	260	265
Arg Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala		270
	275	280
Glu Trp Arg Asn Leu Leu Asp Ser Met Val Leu Ile Thr Asp Lys Phe		285
	290	295
Trp Gly Pro Ser Gly Ala Glu Asn Val Ile Gly Ser Val His Met Trp		300
305	310	315
Leu Ala Glu Ala Ile Asn Ala Leu Gln Asp Asn Lys Asp Thr Leu Thr		320
	325	330
Ala Lys Val Ile Gln Gly Cys Gly Asn Pro Lys Val Asn Pro His Gly		335
	340	345
Ser Gly Pro Glu Glu Lys Arg Arg Arg Gly Lys Leu Ala Leu Gln Glu		350
	355	360
Lys Ser Ser Thr Gly Thr Leu Glu Lys Leu Val Ser Glu Ala Lys Ala		365
	370	375
Gln Leu Arg Asp Ile Gln Asp Tyr Trp Ile Ser Leu Pro Gly Thr Leu		380
385	390	395
Cys Ser Glu Lys Met Ala Met Ser Pro Ala Ser Asp Asp Arg Cys Trp		400
	405	410
Asn Gly Ile Ser Lys Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly		415
	420	425
Leu Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys		430
	435	440
Pro Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr		445
	450	455
Asn Arg Leu Arg Gly Ala Tyr Gly Gly Asn Asp Val Asp Phe Gln Asp		460
465	470	475
Ala Ser Asp Asp Gly Ser Gly Ser Gly Ser Gly Gly Gly Cys Pro Asp		480
	485	490
Asp Ala Cys Gly Arg Arg Val Ser Lys Lys Ser Ser Ser Ser Arg Thr		495
	500	505
Pro Leu Thr His Ala Leu Pro Gly Leu Ser Glu Gln Glu Gly Gln Lys		510
	515	520
Thr Ser Ala		525
530		

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGCTGGGAG GTGTCATTGC TGGAGGCCTG GTGGGCCTCA TCTTTGCTGT GTGCCTGGTG 60  
GCTTTCATGC TATAC 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCCTAGCAG CTGTCATTGC TGGTGGAGTT ATTGGCTTTC TCTTTGCAAT TTTTCTTATC 60  
CTGCTGTTGG TG 72

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Leu Ala Ala Val Ile Ala Gly Gly Val Ile Gly Phe Leu Phe Ala  
1 5 10 15  
Ile Phe Leu Ile Leu Leu Val  
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTGTTGATAG CTGTGATTGT CGGCGGTGTG GTGGGAGCCC TCTTTGCTGC CTTCTTGTGC 60  
ATGCTGCTCA TCTAC 75

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCTTGGCAG CTCTGATTGT GGGCGGCGTA GTGGGCATCC TCTTCGCCGT TTTCCTGATC 60  
CTGCTGCTGG TGTAC 75

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCGCCACTC GCCCAGAGCC TCACTACTTC TTTCTGCTCT TCCTGTTTAC CTTGGTCCTT 60  
GCTGCAGCCA GGCCAGGTG GCGGTAAC TG CCC 93

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Thr Arg Pro Glu Pro His Tyr Phe Phe Leu Leu Phe Leu Phe Thr  
1 5 10 15

Leu Val Leu Ala Ala Ala Arg Pro Arg Trp Arg  
20 25

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGCGACACT GCTCATCCCA GCCATCACGA CTGCTGACGC CGGCTTCTAC CTCTGCGTGG 60  
CCACCAGCCC TGCAGGCACT GCC 83

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCATGAAGA AGAAGGATGA AGGCAGTTAC GACTTGGGCA AGAAACCCAT CTACAAAAAA 60  
GCCCCACCA ACGAGTTCTA CGCATGA 87

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Gly Lys Lys Pro Ile Tyr Lys Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCCGCCAGC AAGAGCCGGA GCT 23

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTGAGGCTCT GGGCGAGTGG GGG 23

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATAGAGCTCT TGAACCATG GCGCCTGTCT GCC

33

- (2) INFORMATION FOR SEQ ID NO:21:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 29 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCCAG GTTTTATTAT CTTTTTATC

29

- (2) INFORMATION FOR SEQ ID NO:22:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 26 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGTATTGGGC GCCGTGTCAC CAGGGC

26

- (2) INFORMATION FOR SEQ ID NO:23:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 26 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCCATGAGC TCCACCACCC TGTTTCG

26

- (2) INFORMATION FOR SEQ ID NO:24:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 9 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Leu Gly Lys Lys Pro Ile Tyr Lys Lys  
1                    5

9

- (2) INFORMATION FOR SEQ ID NO:25:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 4 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Glu Phe Tyr Ala  
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SEP 15 1997